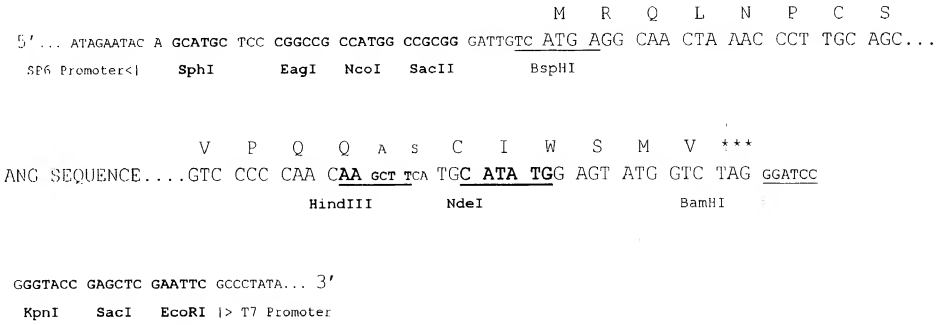


Figure 1

09/743533
PCT/AU99/00563

1
HindIII
oligonucleotide 3
5' CAAGCTTTGAAAGCGCTACTGCGACAGCAGCTGGATCATTGCTTGTGCTATCCGGACTAATACTAGCTGGCACAGTCATAGCA 3'
3' GTTCGAAACTTTCGGCGATGACGCTGTCGTCGACCTAGTAACGAACACGATAGGCCTGATTATGATCGACCGTGTCAGTATCGT 5'
Q A L K A A T A A G S L L V L S G L I L A G T V I A
central anti-parallel beta strands
85
oligonucleotide 4
oligonucleotide 5
5' CTCACAGTGGCCACACCAGTGCTAGTCATATTTAGCCCAGTGCTAGTGCCAGCGGCCATAGCCCTAGCGCTAATGTCAGCAGGC 3'
3' GAGTGTCACCGGTGTGGTCACGATCAGTATAAATCGGGTCACGATCACGGTCGCCGGTATCGGGATCGCGATTACAGTCGTCCG 5'
L T V A T P V L V I F S P V L V P A A I A L A L M S A G
169
234
NdeI
oligonucleotide 6
5' TTTGTCACGTCAGGCGGCGTGGGCTTGGCTGCGCTGAGCTCCTTTAGTGTGTTAGCCAATACTGCCTGCATATGG 3'
3' AAACAGTGCAGTCCGCCGCACCCGACACCGACGCGACTCGAGGAAATCACACAATCGGTTATGACGGACGTATACC 5'
F V T S G G L G V A A L S S F S V L A N T A C I W

Figure 2

```
1
ATGAGGCAACTAAACCCTTGCAGCCAAGAGTTGCAATCACCACAACAATCATATCTGCCG
 M  R  Q  L  N  P Cys S  Q  E  L  Q  S  P  Q  Q  S  Y  L  Q

61
CAGCCATATCCACAAAACCCATATCTACCGCAAAAACCATTTCCAGTGCAGCAACCGTTT
 Q  P  Y  P  Q  N  P  Y  L  P  Q  K  P  F  P  V  Q  Q  P  F

121
CACACACCCCAACAATATTTCCCCTATCTACCAGAGGAATTGTTTCCCCAATATCAAATA
 H  T  P  Q  Q  Y  F  P  Y  L  P  E  E  L  F  P  Q  Y  Q  I

181
CCAACCCCCCTACAACCACAACAACCATTCCCCCAACAACCACAACAACCTCTTCCTCGG
 P  T  P  L  Q  P  Q  Q  P  F  P  Q  Q  P  Q  Q  P  L  P  R

241
CCCCAACAACCATTCCCCTGGCAACCACAACAACCATTTCCCCAGCCCCAAGAACCAATT
 P  Q  Q  P  F  P  W  Q  P  Q  Q  P  F  P  Q  P  Q  E  P  I

301
CCCCAGCAACCACAACAACCATTCCCACAGCAACCACAACAACCATTCCCACAGCAACCA
 P  Q  Q  P  Q  Q  P  F  P  Q  Q  P  Q  Q  P  F  P  Q  Q  P

361
CAACAAATAATTTTCCAGCAACCCCAACAATCATACCCTGTGCAACCTCAACAGCCATTT
 Q  Q  I  I  F  Q  Q  P  Q  Q  S  Y  P  V  Q  P  Q  Q  P  F

421                                                        477
CCTCAACAACCTCAACCAGTCCCCCAACAA GCT TCA TGCATATGGAGTATGGTCTAG
 P  Q  Q  P  Q  P  V  P  Q  Q   A   S  Cys I  W  S  M  V ***
```

Figure 3

HindIII 1 54
AAGCTTCTACCACTCCCACCGCCGTGGCTGTGACTTTCGATCTGACAGCTACCACCACCTAC
A S T T P T A V A V T F D L T A T T T Y

114
GGCGAGAACATCTACCTGGTCGGATCGATCTCTCAGCTGGGTGACTGGGAAACCAGCGAC
G E N I Y L V G S I S Q L G D W E T S D

174
GGCATAGCTCTGAGTGCTGACAAGTACACTTCCAGCGACCCGCTCTGGTATGTCACTGTG
G I A L S A D K Y T S S D P L W Y V T V

234
ACTCTGCCGGCTGGTGAGTCGTTTGAGTACAAGTTTATCCGCATTGAGAGCGATGACTCC
T L P A G E S F E Y K F I R I E S D D S

294
GTGGAGTGGGAGAGTGATCCCAACCGAGAATACACCGTTCCTCAGGCGTGCGGAACGTCG
V E W E S D P N R E Y T V P Q A C G T S

321 NdeI
ACCGCGACGGTGACTGACACCTGGCGGTGCATATGG
T A T V T D T W R C I W

Figure 4

```
HindIII                                                                  57
AAGCTTTCGGCAATGAAGATTGCACCCCATGGATGAGTACTCTGATCACTCCACTCCCAAGC
    A I G N E D C T P W M S T L I T P L P S
CM17. . . . . . . . . . . T . . . . . . . . .

                                                                        117
TGCCGTGACTATGTGGAACAACAAGCATGTCGCATCGAAACGCCCGGGTCGCCGTACCTC
 C R D Y V E Q Q A C R I E T P G S P Y L
 . . N . . . E . . . . . . M . . P . . .

                                                                        177
GCCAAGCAGCAGTGCTGTGGGGAGCTTGCAAACATTCCGCAGCAGTGCCGATGCCAGGCG
 A K Q Q C C G E L A N I P Q Q C R C Q A
 . . . E . . E Q . . . . . . . . . . . . .

                                                                        237
CTGCGCTACTTCATGGGGCCGAAGTCTCGTCCGGATCAGAGCGGCCTCATGGAACTCCCC
 L R Y F M G P K S R P D Q S G L M E L P
 . . . . . . . . . . . . . . . . . . . .

                                                                        297
GGATGCCCTAGGGAGGTGCAGATGGACTTCGTGAGGATACTCGTCACGCCGGGGTACTGC
 G C P R E V Q M D F V R I L V T P G Y C
 . . . . . . . . N . . P . . . . . . . .

                                                                    354
AACTTGACGACCGTTCACAACACTCCGTACTGCCTCGCTATGGAGGAGTCTCAGTGG
 N L T T V H N T P Y C L A M E E S Q W
 . . . . . . . . . . . . G . . . . . .

357   NdeI
AGCTGCATATGG
 S C   I W
```

Figure 5

```
HindIII                                                              57
AAGCTTACGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTGTAGAGACAAAGCTAAAT
  A  Y  D  V  A  G  G  G  G  A  Q  Q  C  P  V  E  T  K  L  N

                                                                    117
TCATGCAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGG
 S  C  R  N  Y  L  L  D  R  C  S  T  M  K  D  F  P  V  T  W

                                                                    177
CGTTGGTGGAAATGGTGGAAGGGAGGTTGTCAAGAGCTCCTTGGGGAGTGTTGCAGTCGG
 R  W  W  K  W  W  K  G  G  C  Q  E  L  L  G  E  C  C  S  R

                                                                    237
CTCGGCCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGAT
 L  G  Q  M  P  P  Q  C  R  C  N  I  I  Q  G  S  I  Q  G  D

                                                                    297
CTCGGTGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAG
 L  G  G  I  F  G  F  Q  R  D  R  A  S  K  V  I  Q  E  A  K

                                                                    300
AACCTGCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTAT
 N  L  P  P  R  C  N  Q  G  P  P  C  N  I  P  G  T  I  G  Y

   363   NdeI
TACTGGTGCATATGG
 Y  W  C  I  W
```

Figure 6

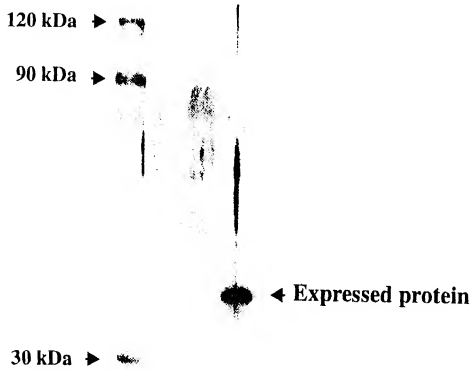
Figure 7

Figure 8

Figure 9

Figure 10

Figure 11



A B C D

Figure 12

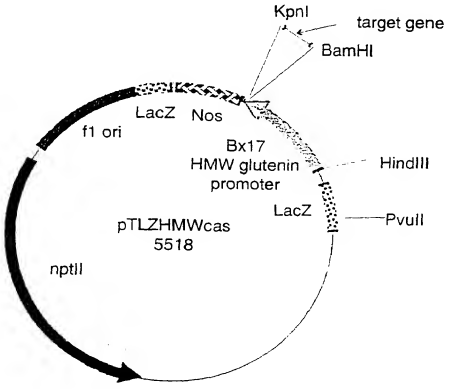

KpnI
target gene
BamHI
LacZ
Nos
f1 ori
Bx17
HMW glutenin
promoter
HindIII
LacZ
PvuII
pTLZHMWcas
5518
nptII

Figure 13

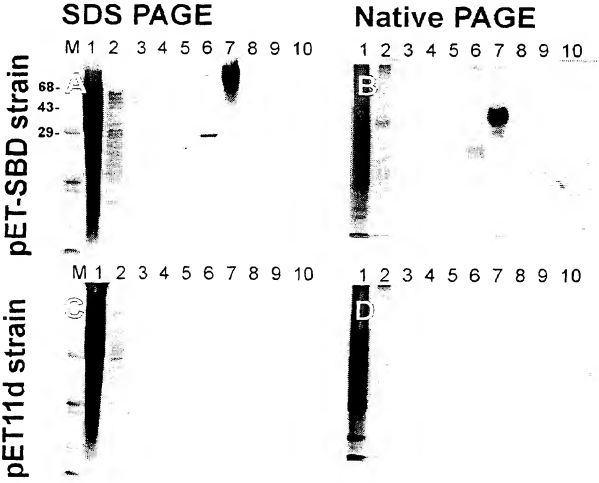

SDS PAGE
Native PAGE
M 1 2 3 4 5 6 7 8 9 10
1 2 3 4 5 6 7 8 9 10
pET-SBD strain
pET11d strain
68-
43-
29-
A
B
C
D

Figure 14

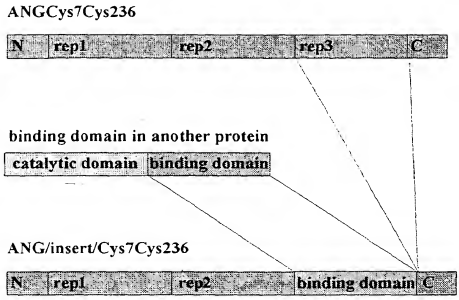


Figure 15

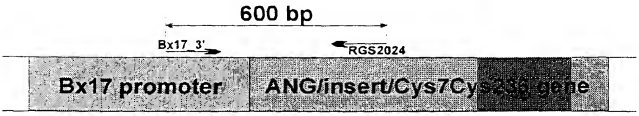


Figure 16

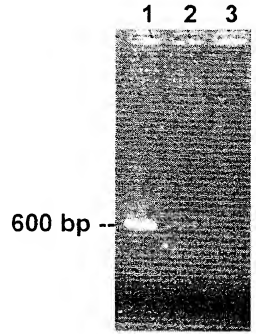


Figure 17

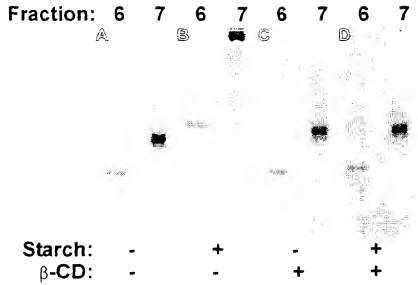


Figure 18

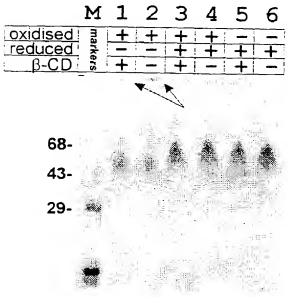


Figure 19